

GenCore version 5.1.4-p5_4578
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model.

Run on: March 11, 2003, 03:30:16 ; Search time 5816 Seconds
(without alignments)
16683.073 Million cell updates/sec

Title: US-10-046-433-39
Perfect score: 3334
Sequence: 1 gtagaaggcagcgcgcgc... attaaaaaaaaaaaaaa 3334

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank:
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41: em_htgo_other: *

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3303.4	99.1	3501	6 AX463904	AX463904 Sequence
2	3259.6	97.8	3280	6 AX03667	AX03667 Sequence
3	3258.8	97.7	3331	6 AX127726	AX127726 Sequence
4	2726.5	81.8	2733	6 AX127740	AX127740 Sequence
5	2603.6	78.1	2610	6 AX127742	AX127742 Sequence
6	2603	78.1	2895	9 AK057647	AK057647 Homo sapi
7	2227	66.8	2449	9 BC031648	BC031648 Homo sapi
8	2094.4	62.8	2129	9 AK026832	AK026832 Homo sapi
9	1938	58.1	5567	9 AB037745	AB037745 Homo sapi
10	1705	51.1	1717	6 AX03071	AX03071 Sequence
11	1145.8	34.4	1149	6 AX127746	AX127746 Sequence
12	1008.8	30.3	1587	6 AX213277	AX213277 Sequence
13	951.8	28.5	1119	6 AX213279	AX213279 Sequence
14	834.4	25.0	1149	10 BC026555	BC026555 Mus muscu
15	807.8	24.2	3185	9 AK05902	AK05902 Homo sapi
16	641.4	19.2	677	6 AX036669	AX036669 Sequence
17	625.4	18.8	627	6 AX127744	AX127744 Sequence
18	537.6	16.1	1737	6 AX060311	AX060311 Sequence
19	537.6	13.3	443	6 AX127734	AX127734 Sequence
20	424.4	12.7	426	6 AX368203	AX368203 Sequence
21	419.8	12.6	1508	6 AX060301	AX060301 Sequence
22	399	12.0	480	6 AX182004	AX182004 Sequence
23	382.6	11.5	437	6 AX182039	AX182039 Sequence
24	346	10.4	373	6 AX070263	AX070263 Sequence
25	343.4	10.3	353	6 AX182022	AX182022 Sequence
26	337.2	10.1	399	6 AX182000	AX182000 Sequence
27	292.2	8.8	97114	2 AL157901	AL157901 Human DNA
28	292.2	8.8	116603	2 AL157901	AL157901 Human DNA
29	284.4	8.5	466	6 AX261103	AX261103 Sequence
30	282.4	8.5	306	6 AX37557	AX37557 Sequence
31	263.4	7.9	265	6 AX368154	AX368154 Sequence
32	261	7.8	316	6 AX098150	AX098150 Sequence
33	242.4	7.3	304	6 AX098167	AX098167 Sequence
34	240	7.2	2188	10 BC029010	BC029010 Mus muscu
35	214.2	6.4	89129	10 AL672200	AL672200 Mouse DNA
36	214.2	6.4	19886	2 AL683823	AL683823 Mus muscu
37	211.2	6.4	23154	2 AC093365	AC093365 Mus muscu
38	210	6.3	146336	2 AC011645	AC011645 Homo sapi
39	208.4	6.3	45557	9 AL138933	AL138933 Human DNA
40	199	6.0	16800	2 AC113756	AC113756 Rattus no
41	189.6	5.7	231	6 AX302725	AX302725 Sequence
42	171	5.1	171	6 AX127730	AX127730 Sequence
43	162.8	4.9	404	6 AX071721	AX071721 Sequence
44	162	4.9	164800	2 AC113756	AC113756 Rattus no
45	158	4.7	158	6 AX127732	AX127732 Sequence

ALIGNMENTS

TITLE		Wood, W.-L. and Zhang, Z.	
JOURNAL		Secreted and transmembrane polypeptides and nucleic acids encoding	
PATENT: WO 0140466-A 37 07-JUN-2001;		same	
Genentech Inc. (US)		Genentech Inc. (US)	
FEATURES	source	Location/Qualifiers	
1. 3501	/organism="Homo sapiens"		
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Qy	2041	CGCAACACTCACCAGAACAGATCCTACTCTCTGTCATACTGATGCCACTTCTCA	2100
Db	2116	CGCAACACTCACCAGAACAGATCCTACTCTCTGTCATACTGATGCCACTTCTCA	2175
Qy	2101	CTTGCTGGAGGCCAGCTACTCTGTCATACTGATGCCACTTCTCA	2160
Db	2176	CTTGCTGGAGGCCAGCTACTCTGTCATACTGATGCCACTTCTCA	2235
Qy	2161	AGTCCTGTTGAAACCGGGTAGGAAATGTCGTTGTCACCCACAAATGTCGTTGACCT	2220
Db	2236	AGTCCTGTTGAAACCGGGTAGGAAATGTCGTTGTCACCCACAAATGTCGTTGACCT	2295
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Qy	2341	CTTGCTGTTGAAACCGGGTAGGAAATGTCGTTGTCACCCACAAATGTCGTTGACCT	2400
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Qy	2941	GCCATCATGGAAGGGAGTATGAGGACCCATCTTACAGCAGAA-TCACTG	2999
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Qy	3000	TTGGGAAGTCAATCTTACCTGGAGGACTCTGATGGATTGACTCTGGCC	3059
Db	3076	TTGGGAAGTCAATCTTACCTGGAGGACTCTGATGGATTGACTCTGGCC	3135
Qy	3060	CTGAAGACATCTCAGGAGGCCAGACATGACCTGTGAGGAGCTGCCCTGCCTCACCT	3119
Db	3136	CTGAAGACATCTCAGGAGGCCAGACATGACCTGTGAGGAGCTGCCCTGCCTCACCT	3195
Qy	3120	GCCTCTCACCTTGCAATGACCTTGGCAAGCCATTGGTGCAGATCTCA	3255
Db	3196	GCCTCTCACCTTGCAATGACCTTGGCAAGCCATTGGTGCAGATCTCA	3239
Qy	3180	CAACACCACTGCTGAAATCTCTCATGTTGCGCTTATCAGATGTTGATTCAGTC	3315
Db	3256	CAACACCACTGCTGAAATCTCTCATGTTGCGCTTATCAGATGTTGATTCAGTC	3299
Qy	3240	TTTTTTATGAGTACCCAAACCTCTTCGCTGCTGCCTCRAACTGCCAAATATACCC	3375
Db	3316	TTTTTTATGAGTACCCAAACCTCTTCGCTGCTGCCTCRAACGCCAAATATACCC	3375
Qy	3300	ACACTTGTGTTGAAATTAAAAAAATAAAAAA 3334	
Db	3376	ACATTTTTAAAAAAAAATAAAAAA 3410	

QY	2578	TGTGATGGCCTGCAACTTCACTTCTGTTGGAGAACGGCGGGCTCTGCCGCTCTGCTCA	2637	CDS
Db	2521	TGTGATGGCCTGCAACTTCACTTCTGTTGGAGAACGGCGGGCTCTGCCGCTCTGCTCA	2580	
QY	2638	GTGGCTGACTACATCGTATCGTCAGCAGCTGTTGGGGATCTCTGCTGAGAGACTACTAC	2697	
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Db	2701	ATCTGCAAAACCATAGATTCCTGGCTGAAAGTGGCATCTCGGCTGAGAGACTAC	2760	
QY	2818	ATCTGCTGACCGCTGTTGACTCTACTTGTGAAAGAATAAACCTAGGTAG	2877	
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QY	2878	TACTCCAAAGCTGGTGTGATGATGCTACTCTCAAGACTGTGACCTGGCCAGCAGTGAC	2937	
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QY	2938	TGGCCCATCANGGAAGCGAGATAGAGGACCTCTTACAGCAAGAA-TCA	2996	
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QY	2997	CTCTTGGGAGAATCAATTATTCACCTCCAGGAGCTCTTACAGCAAGAGTCA	3056	
Db	2941	CTCTTGGGAGAATCAATTATTCACCTCCAGGAGCTCTTACAGCAAGAGTCA	3000	
QY	3057	CCGCTGAGACATCCCTCAGGAGCCAGACATGGACCTGTGAGGGACTGCTGCCPCA	3116	
Db	3001	CCGCTGAGACATCCCTCAGGAGCCAGACATGGACCTGTGAGGGACTGCTGCCPCA	3060	
QY	3117	CCTGCTCTGACCTGCTAGCACCTTGGCAAGCCCTGGGCAAGTGGCTGAGCATC	3176	
Db	3061	CCTGCTCTGACCTGCTAGCACCTTGGCAAGCCCTGGGCAAGTGGCTGAGCATC	3120	
QY	3177	CTGCAACACCCACTGCTGGAAATCTCTCTGTCAGATGTTGAAATTGAG	3236	
Db	3121	CTGCAACACCCACTGCTGGAAATCTCTCTGTCAGATGTTGAAATTGAG	3180	
QY	3237	ATCTTTTATAGTACCAACCTCTTCGCTGCTCCAAACTTGCCAAATA	3296	
Db	3181	ATCTTTTATAGTACCAACCTCTTCGCTGCTCCAACTTGCCAAATA	3240	
QY	3297	CCACACTTGTGTAATAAaaaaaaaaaaaaaa	3334	
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DEFINITION				
ACCESSION	AZ127726			
VERSION	AZ127726.1			
KEYWORDS	human.			
SOURCE	Organism			
Eukaryote;	Metazoa;	Chordata;	Craniata;	Vertebrata;
Mammalia;	Eutheria;	Primates;	Catarrhini;	Hominidae;
REFERENCE	1 (bases 1 to 331)			Homo.
AUTHORS	Delneste, Y., Magistrelli, G., Jeannin, P. and Bonnefoy, J.Y.			
TITLE	Cloning, expression and characterisation of a gene expressed in			
JOURNAL	tumour cells and involved in the regulation of the immune response			
PATENT	WO 0131003 A 1 03-MAY-2001;			
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QY	1078	CTCTGCTGAGGGCCAGCTCAGTCACCTCCAAAGGGTGAAGAAAGTCTGTCACCTTAC	11020	Db	2101	CTCACTCTCTGGAACACGGGTAGGAAATGTCAGTCACCTTAC
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QY	1918	ATCTGCAAAACATAGATTCTGGCTGAGTG	1860	Db	2758	ATCTGCAAAACATAGATTCTGGCTGAGTG
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RESULTS

5 AXI:27742

LOCUS AXI:27742

DEFINITION Sequence 17 from Patent WO0131003.

ACCESSION AXI:27742

VERSION AXI:27742.1

KEYWORDS GI:14134389

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Maitreya, S. L.; Eutheria; Primates; Catarhini; Hominoidea; Homo.

AUTHORS 1 (bases 1 to 2610)

TITLE Delestre, Y.; Magistrelli, G.; Jeannin, P. and Bonnefond, J.Y. Cloning, expression and characterisation of a gene expressed in tumour cells and involved in the regulation of the immune response

JOURNAL Patent: WO 0131003 A1 17 03-May-2001; PIERRE FABRE MEDICAMENT (FR)

FEATURES Location/Qualifiers

source 1 - 2610

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Quary	Match	78	1%	Score	2603	6	DB	6	Length 2610;		
Best Local Similarity	99	8%	Pred.	No.	0;	Mismatches	4;	Indels	0;		
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Qy	241	GACAGCACGCGTCCAGGTAGGAGGCTCGCCGTCGCGCATCCCCGGCGCTGTGACCGAGC	300	Qy	241	GATATGAGGACAGCAGTCATGAGGCTGAGGGCGCATACCCGGCCGTGACCGAGC	120	Db	1321	GAATACAATGGGGACACGCTGAGGACTGAGCTGCTGAGGACTGAGCTGCTGTT	1380
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Qy	481	GAGCTGGATGACAGTGTCTGAGTACCTGAGCTGAGCTGAGCTGAGCTGAGCT	540	Qy	1621	AACACTCTGTGAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT	1680	Qy	1681	GAGGAGACACTACCGAGCTGGGGACTGAGCTGAGGAGCTGAGCTGAGCTGAGCT	1740
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Qy	661	TGTGAGTTCTGTCAGATGAGCTGAGCTGAGCTGAGCTGAGCT	720	Qy	1741	CCCGCTACATTTGAGGAGCTGAGCTGAGCTGAGGAGCTGAGCTGAGCTGAGCT	1800	Qy	1921	CCCGCTACATTTGAGGAGCTGAGCTGAGGAGCTGAGCTGAGCTGAGCTGAGCT	1980
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Db	1921	CTTGCTGGAGGGCAGCTTCACCTGAGCTTCACTACACTTCCTCCACT	2100	NEDO human cDNA sequencing project
Db	2161	AGTCCTGTGAAACAGGGTAGGAAAGTCTGTCAGCGAGATGCACCTC	2120	unpublished
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Db	2221	GGGATCTCTGAGGGTGAATGCTGACCGAGATGCTGACCGAGCTAC	2240	direct submission
Qy	2041	GGGATCTCTGAGGGTGAATGCTGACCGAGCTACGGCTACGGCTAC	2280	Submitted (24-OCT-2001) Takeo Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 299-0812, Japan (E-mail:genomics@nti.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
Db	2101	GTCACTACCCAGAGGTGACAGCTACAGCTACAGCTACGGCTAC	2100	NEDO human cDNA sequencing project
Qy	2341	CTTGCTGTGACTATGGGTGACAAGATATGACTCTGGATGAAATC	2400	ECONOMY, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan KEY Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.
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RESULT 6				
AK057647	AK057647	Homo sapiens cDNA FLJ33085 2895 bp mRNA linear PRI 01-AUG-2002	1.	
DEFINITION		to MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR.		
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VERSION	AK057647.1	oligo capping, f1s (full insert sequence), clone.lib:TRACH2		
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SOURCE		clone:TRACH200420.		
ORGANISM		Homo sapiens		
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS		Shiokawa,N., Matsunaga,Y., Moriya,S., Chiba,E., Momiyama,H., Onogawa,S., Kaeiyama,S., Satoh,N., Matsunawa,H., Takahashi,E.,		

Db	503	GAGCTGGATGACAGTGTCTGAGTCCACCGGGAACTGTACTTCGTTCCAAGTGGTTCCC	562	Qy	1621	AAQACTCTGTGGAGACGTGGAAAGTTCCAAGGAAACAGTCCTATACCATCATT	1680
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Qy	841	AGAACATTCGGCATACAGGGTGGCTCACTCTCAGAATGCTTCCCTGCAAACT	900	Db	1853	GGTCAGGGACCAAGAACACAGCCACCCATGAGCCACACGGCTTATGGTTCAGGCTG	1852
Db	880	-	-	Qy	1793	CCCAACACTCCACCCAGGAGTTCACTACAACTCTCGCTTGGCAACACCGTCACT	2100
Qy	961	ATAAAGGAGAACTCTGGCCACAGCTGCACAGACAAAGATTATTCAGACAA	1020	Db	1913	CCCAACACTCCACCCAGGAGTTCACTACAACTCTCGCTTGGCAACACCGTCACT	1972
Db	893	TCTTCTGTAACGTCGCCACCTTSCACAGACAAAGATTATTCAGACAA	1020	Qy	2101	ACRPTCTGGAGGSCCAAGCTTACTCCAAAGGGTGAATACTTCATCATCTGACTC	2160
Db	880	-	-	Qy	1981	GGTCAGGGACCAAGAACACAGCCACCCATGAGCCACACGGCTTATGGTTCAGGAACTGGCACTCTG	1912
Qy	1021	TCTTCTGTAACGTCGCCACCTTSCACAGACAAAGATTATTCAGACAA	1080	Db	1853	CTGTCGAGGGCCAAAGCTTACTTCAGACAAAGTCCACTCTGTCAGTGCACCTCTC	2032
Qy	1081	TGCAATGCGAACAGAGAACACTCATGACAAATGGCCAAAGCAGTGTAC	1140	Qy	2041	CCCAACACTCCACCCAGGAGTTCACTACAACTCTCGCTTGGCAACACCGTCACT	2100
Db	953	TGCGATGCCAACGGAGAGAACACTCATGACAAATGGCCAAAGCAGTGTAC	1012	Db	1913	CCCAACACTCCACCCAGGAGTTCACTACAACTCTCGCTTGGCAACACCGTCACT	1972
Qy	1141	GAGGAGCTTGTGGGGAGTGTAGCTGCTCTGGTGAGAACCCCCACTGCCAC	1200	Db	2101	CTGTCGAGGGSCCAAGCTTACTCCAAAGGGTGAATACTTCATCATCTGACTC	2220
Db	1013	GAGGAGCTTGTGGGGAGTGTAGCTGCTGCTCTGGTGAGAACCCCCACTGCCAC	1072	Qy	2161	ACRPTCTGGAGGAAATGTTCTGTCAGGCAATGTCAGTTCCTGACTGACTC	2092
Qy	1201	TGCAACCCAGGTCTTCAAAACAAACACACACACACACACACACACAC	1260	Db	1973	CTGTCGAGGGCCAAAGCTTACTTCAGACAAAGTCCACTCTGTCAGTGCACCTCTC	2032
Db	1073	TGCAACCCAGGTCTTCAAAACAAACACACACACACACACACACACAC	1132	Qy	2231	GGATTCTGTGGGTGAGTGTAGGTCAGACGGCTCACAGCCGGGTTCCACAGCTGACCTCTC	2280
Qy	1261	TACTCCATGGCTCAGCTGTACCGTCGCCCTGCGAGGACTGAACCGTGTGGATT	1320	Db	2153	GGATTCTGTGGGTGAGTGTAGGTCAGACGGCTCACAGCCGGGTTCCACAGCTGACCTCTC	2212
Db	1133	TACTCCATGGCTCAGACTGTACCCGCTGCCCTGCGAGGACTGAACCTGTGGATT	1192	Qy	2221	GGATTCTGTGGGTGAGTGTAGGTCAGGGTCTCCAAATCTACACAGCCTACGGCTGAGGCA	2152
Qy	1321	GTATAAACATGGTGGACACGCCCTGCCACAAACATGGAAACACCGTCTCGTGGATC	1380	Db	2093	CGGATTCCTGGAGGTGAGTGTAGGTCATCCAAATCTACAGCTTGTGCAAGCA	2152
Db	1193	GTATAAACATGGTGGACACGCCACAAACATGGAAACACCGTCTCGTGGATC	1252	Qy	2281	GTATCATTCCCCCAGGGTGAAGGCTACAGGGGGGTTCCACAGCTGCTGTCAG	2340
Qy	1381	AACTGGAGTACAGGGCATGACAGCTGGGGAGTGGTGTGATCACATTACAGCT	1440	Db	2213	CTGTCGAGCTTATGGGTGACACAGATATGACTCTGTCAGTGTGAAATACCTCCCA	2272
Db	1253	AACTGGAGTACAGGGCATGACAGCTGGGGAGTGGTGTGATCACATTACAGCT	1312	Qy	2341	CTGTCGAGCTTATGGGTGACACAGATATGACTCTGTCAGTGTGAAATACCTCCCA	2400
Qy	1441	GTGTTGGAGCTTACAGACATGACTCTGCTTCACCTCTGGTGTGGAGGTTAGCT	1500	Db	2213	CTGTCGAGCTTATGGGTGACACAGATATGACTCTGTCAGTGTGAAATACCTCCCA	2272
Db	1313	GTGTTGGAGCTTACAGACATGACTCTGCTTCACCTCTGGTGTGGAGGTTAGCT	1372	Qy	2401	GCTGAGCTTTCACCTGGAGTCTGGGAATACCGGACTCTGTCAGTGTGAAATACCTCCCA	2460
Qy	1501	CCCGAGCTGGTGTGGAGACAGACAGAGAAAGGGTGGCCAGATCAGTGTG	1560	Db	2273	GCTGAGCTTTCACCTGGAGTCTGGGAATACCGGACTCTGTCAGTGTGAAATACCTCCCA	2332
Db	1373	CCCGAGCTGGTGTGGAGACAGACAGAGAAAGGGTGGCCAGATCAGTGTG	1432	Qy	2461	AATGATGTTACCCAGTGTCTGGAGTGTGAGTGTGAAATACCTCCCA	2392
Qy	1561	GAGACCCCTGTCTGTGAACTGTGACTCTACTCATGGGGGTGTGATCTAGGACC	1620	Db	2513	GCTGACTTACATGTGTCAGCAGCTGGTGTGAAAGTCAACCCACATCCCGCTG	2572
Db	1433	GAGACCCCTGTCTGTGAACTGTGACTCTACTCATGGGGGTGTGATCTAGGACC	1492	Qy	2453	GATGGCTGCAACTTCACCTCTGGAGAGCAGGGGTGCTCCAGGAGTCACTTACCTG	2512

Qy	2701	TGGCGAGAACCCAAAGCTATCCTCTGGGCATTCCTCTGCCTTAGCAGAGCTTACCATC	2760	OPCPYGSYNSGSDCTRCPASHEPAYGFEYKWWNTLPTNMEITLUSINEYKGMGTWE
Db	2573	TGGCGAGAACCCAAAGCTATCCTCTGGGCATTCCTCTGCCTTAGCAGAGCTTACCATC	2632	VAGDHLYTAGASDNDMILTLVPGFPRPQSVMDAERKEVANITYFPEFLSVNDE
Qy	2761	TGCAAAACCATAGATTTCTGGCTTAAGGGGATCTCGAGCAGCCTGACTGCCATC	2820	LIFMVEVNSRNPDEPNTVPEKQSKGKSYTTIENNTSTWAFRTTHPEASVYND
Db	2633	TGCAAAACCATAGATTTCTGGCTTAAGGGGATCTCGAGCAGCCTGACTGCCATC	2692	VAKTYSINTVNMVNGVASCRCPALEASDWSCTSPGYYIDYRDSCTCHSCPPNTI
Qy	2821	CTGCTTACCGTCTGACCTGCTACTTTGGAAGAACACTAACAGTAGATCAGAAGT	2880	GPFSTSKGLKFHRTLSLGGNQGRKMSVCTDNVMDLRTGTCDFNCFNHLWESACPL
Db	2693	CTGCTTACCGTCTGACCTGCTACTTTGGAAGAACACTAACAGTAGATCAGAAGT	2752	SNDVPOSCSGRSRTPTRVCSPOKTPGSSLLRCDFCSDTCDGCNFRHILWESACPL
Qy	2881	TCCAGCTGCTGTAAGTCTCAAGGACTGTGACTC	2921	CSVADYHATVSCVAGIQITYWREPKLCSGGISLPRORVTTICKTIDFWLKVG
Db	2753	TCCAGCTGCTGTAAGTCTCAAGGACTGTGACTC	2793	TCTAATLTWVTCYTMKKNRLEYKSKLMMATLKDCLDPAADSCTAIMEGENVEDDIL
				FTSKSLRKTSKTPDGDSEPVMTSSGGRDMDL
RESULT	7			BASE COUNT
LOCUS	BC031648	2449 bp mRNA	lineар	618 a
DEFINITION	Homo sapiens, KIAA1324 protein, clone MGC:35166 IMAGE:516952,		PRI 26-JUN-2002	690 c
ACCESSION	BC031648			563 g
VERSION	BC031648.1			578 t
KEYWORDS	MGC.			
SOURCE	human.			
ORGANISM	Homo sapiens			ORIGIN
REFERENCE			Query Match	66.8%; score 2227; DB 9; Length 2449;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Best Local Similarity	100.0%; Pred. No. 0;
TITLE	1 (bases 1 to 2449)		Matches	2238; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
JOURNAL	Direct Submission		Qy	1097 AGACACAACTCATGACAAATGGCCACCGAACATTGAGGACCTGAGGGGG
INSTITUTE	Submitted (06-JUN-2002) National Institutes of Health, Mammalian		Db	197 AGACACAACTCATGACAAATGGCCACCGAACATTGAGGACCTGAGGGGG
USA	Gene Collection (MGC), Cancer Genomics Office, National Cancer		Qy	1157 CAGCGAAGCTGCCCTCTGTTGAGAACGCCACTGCCACCCCTGCACCCAGGCTCT
REMARK	NIH-MGC Project url: http://mgc.nci.nih.gov		Db	257 CAGTGAAAGCTGCCCTCTGTTGAGAACGCCACTGCCACCCCTGCACCCAGGCTCT
COMMENT	Contact: MGC help desk		Qy	1217 TCAAAACCAACAGACCTGGCAGCCTGCCACCGCTGCCATATGGTGTGAA
	Email: cgaps-r@mail.nih.gov		Db	317 TCAAAACCAACACAGACCTGGCAGCCTGCCACCGCTGCCATATGGTGTGAA
	Tissue Procurement: Life Technologies, Inc.		Qy	1277 ACTGTTACCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG
	cDNA Library Preparation: Life Technologies, Inc.		Db	377 ACTGTTACCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG
	cDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL)		Qy	1337 ACACGCTGCCAACAAATGAAACGACCGCTCTGAGGATCACTCGAGCATACTCGAG
	DNA Sequencing by: Baylor College of Medicine Human Genome		Db	437 ACACGCTGCCAACAAATGAAACGACCGCTCTGAGGATCACTCGAGCATACTCGAG
	Sequencing Center		Qy	1397 GCATGAGAGGCTGGGGAGGTGGCTGGCATCACATTACAGCTGAGCTGAGCTGAG
	Center code: BCM-HGSC		Db	497 GCATGAGAGGCTGGGGAGGTGGCTGGTGTGATCACATTACAGCTGAGCTGAGCTGAG
	Web site: http://www.hgsc.bcm.tmc.edu		Qy	1457 ATGACTCTCATGTTCTACTCTGGTGTGAGGATTTAGCCCTGGCTGGTGTGAG
	Contact: ang@bcm.tmc.edu		Db	557 ATGACTCTCATGTTCTACTCTGGTGTGAGGATTTAGCCCTGGCTGGTGTGAG
	Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,		Qy	1517 CAGACACAGAGATAAAGAGGTGGCAGAACATTTGCTTTAGACGCCCTGCTG
	Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,		Db	617 CAGACACAGAGATAAAGAGGTGGCAGAACATTTGCTTTAGACGCCCTGCTG
	Richards, S., Gibbs, R.A.		Qy	1577 TGACTCTGACCTCACTCTGGGGTGTGAATTCAGGACCAACACTCCCTGGGAGA
	Clone distribution: MGC clone distribution information can be found		Db	677 TGACCTGTGAGCTCTACTCATCTGGGGTGTGAATTCAGGACCAACACTCCCTGGGAGA
	through the T.M.A.G.E. Consortium/INTL at: http://image.lnl.gov		Qy	1637 CGTGGAAAGCTCCAAAGGAAACAGTCTTACCTACATCTGGAGGAGACTACCA
	Series: IRAK Plate: 51 Row: d Column: 23		Db	737 CGTGGAAAGCTCCAAAGGAAACAGTCTTACCTACATCTGGAGGAGACTACCA
	This clone was selected for full length sequencing because it		Qy	1697 CGAGCTTCACTGGCCCTTCAGGAGGACCACTTTCAGGAGCAAGAGGAAGTACCA
	passed the following selection criteria: Hexamer frequency ORF		Db	797 CGAGCTTCACTGGCCCTTCAGGAGGACCACTTTCAGGAGCAAGAGGAAGTACCA
	analysis.		Qy	1757 ATGAGCTTCACTGGCCCTTCAGGAGGACCACTTTCAGGAGCAAGAGGAAGTACCA
FEATURES	Location/Qualifiers		Db	857 ATGAGCTTCACTGGCCCTTCAGGAGGACCACTTTCAGGAGCAAGAGGAAGTACCA
source	1. .2449		Qy	1817 ACTGCCGCTCTGGCCCTAGAGCCCTTGAGTGGCTCCCTGACCTCTGCTG
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Qy	1216	TTCAAACACAAACAGACACCTTGCCATAGGCCATATGGCTCTACTCCATGGCA	1275						
Db	14	TTCAAAACACAAACAGACACCTTGCCATATGGCTCTACTCCATGGCA	73						
Qy	1276	GACTGTACCGCTGCCCTCGAGGACTGACCTCTGTTGATACAAATGGTG	1335						
Db	74	GACTGTACCGCTGCCCTCGAGGACTGACCTCTGTTGATACAAATGGTG	133						
Qy	1336	ACACAGCTGCCAACACATGGAAACGACCGTCTCACTGGAGACAC	1395						
Db	134	ACACAGCTGCCAACACATGGAAACGACCGTCTCACTGGAGACAC	1395						
Qy	1395	GGCATGACAGCTGGAGGTGTTGATCACAGCTGCTGGGATGACAG	193						
Db	254	ATGGACTCATATTCCTACTCTGGTGTGCGGAGATCACAGCTGCTGGGATGACAG	193						
Qy	1516	GCAGACAGAGATAAAGAGGTGGCAGAATCACATTGTTGAGACCCCTGACT	1455						
Db	314	GCAGACAGAGATAAAGAGGTGGCAGAATCACATTGTTGAGACCCCTGACT	1575						
Qy	1576	GGAGACTGTGAGCTCTACTCATGGGGGTGATTCTAGGCCAACACTCTGTGAG	1635						
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Qy	1636	AGTGGAAAGTCTCAAAAGCAACAGCTTCTAGGCAAGCAGGAGACACTACC	1695						
Db	434	AGTGGAAAGTCTCAAAAGCAACAGCTTCTAGGCAAGCAGGAGACACTACC	1695						
Qy	1696	ACGAGGTTTCACTTGGCCCTGCCAGGACACTTCTAGGCAAGCAGGAGTACCC	493						
Db	494	ACGAGGTTTCACTTGGCCCTGCCAGGACACTTCTAGGCAAGCAGGAGTACCC	1755						
Qy	1756	AACTGAGGTGCAAGATCTACTCATCATGACATGTTGAAATGGGTGSCCTC	1815						
Db	554	AACTGAGGTGCAAGATCTACTCATCATGACATGTTGAAATGGGTGSCCTC	613						
Qy	1816	TACGCCGRCCTGTGCCCTAGGCTCTGAGGCTCTGAGTGTGGCTCCTGACCTCTGCT	1875						
Db	614	TACGCCGRCCTGTGCCCTAGGCTCTGAGGCTCTGAGTGTGGCTCCTGACCTCTGCT	1875						
Qy	1876	GGGGTTACTATTTGACCGAGATTCAGGAACTTGCACACTCTGCCCTTAACAAATT	1935						
Db	674	GGGGTTACTATTTGACCGAGATTCAGGAACTTGCACCTCTGCCCTTAACAAATT	1935						
Qy	1936	CTGAAAGCCACAGCCATTGTCAGGCCCTGGTCCAGGGACAG	1995						
Db	734	CTGAAAGCCACAGCCATTGTCAGGCCCTGGTCCAGGGACAG	793						
Qy	1996	ACGACAGATCCACTCTCTGCTCACATTGACCAACACTCCAC	2055						
Db	794	ACGACAGATCCACTCTCTGCTCACATTGACCAACACTCCAC	733						
Qy	2056	AGCAGTCTCACTAACTCTCCCTTGCCAAACACCGTCACTCTGCTGAGGGCA	853						
Db	854	AGCAGTCTCACTAACTCTCCCTTGCCAAACACCGTCACTCTGCTGAGGGCA	2115						
Qy	2116	AGCTTCACTTCAAAAGGTGAATACTCTACACTTACCTCTGTTGAGAC	2175						
Db	914	AGCTTCACTTCAAAAGGTGAATACTCTACACTTACCTCTGTTGAGAC	973						
Qy	2176	CAGGTAGGAATCTCTGTCAGGACCCACAAATGCTACTGCTACTCTGCTGAGGGT	2235						
Db	974	CAGGTAGGAATCTCTGTCAGGACCCACAAATGCTACTGCTACTCTGCTGAGGGT	2235						
Qy	2236	GAGTCAGGGTTCTCAAACTCATACGCTCTGCTGAGGCTCATCCACCA	2295						
Db	1034	GAGTCAGGGTTCTCAAACTCATACGCTCTGCTGAGGCTCATCCACCA	1093						
Qy	2296	GAGGTGACAGCTACAGGCCGGGGTTCTCACAGCCTTGCTGAGCTT	2355						
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Qy	2356	ATGGGGTACACAGATAATGACTCTGATGATGAACTACCTCCAGCTGAGCTT	2415						
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Qy	2416	CTGGAGTCTTGGAAATACCGGCTCTGAGTCACTTGAGTACAAC	2475						
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Qy	2476	TCCMGCAGTCTGGAGATCACACCCATGGGCTAGGTCAGCCAG	2535						
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Qy	2536	CTTGGAAATGCTCTGCGAGGTTGACCCCTGTTGAGACCCCTGCT	2595						
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Qy	2596	CACTCTCTGGAGAGACATACCCATGGGCTAGGTCAGTCCAGT	2655						
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Qy	2656	ATCGTCAGCACTGTTGGGGATCCAGGCCAACACTCTGTGAG	2715						
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Qy	2716	CTATCTCTGGGATTCCTGCTGCTGCTGCTGCTGCTGCTGCT	2835						
Db	1514	CTATCTCTGGGATTCCTGCTGCTGCTGCTGCTGCTGCTGCT	2775						
Qy	2776	TTCGGCTGAAAGTGGCATCTCTGCTGCTGCTGCTGCTGCTGCT	2835						
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Qy	2836	ACCTGCTACTTTGGAAAAAGATCACAAACTAGTACAGTACTCCAGCTGTTGATG	2895						
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Qy	2896	AACTGCTACTCTCAAGGACTCTGACCTGACCTGACAGCTGACTT	2955						
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Qy	3015	TCTTTCACCTCAAGGACTCTGACCTGACCTGACAGCTGACAG	3074						
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Qy	3075	GGAGGCCAGACATGGACCTGAGGACACTCTGCTCCCTGCTCCCTGCT	3134						
Db	1874	GGAGGCCAGACATGGACCTGAGGACACTCTGCTCCCTGCTCCCTGCT	1933						
Qy	3135	ATAGACCTTGCTGACCTGCGGCTATGAGCTGAGGAGCTGAG	3194						
Db	1934	ATAGACCTTGCTGACCTGCGGCTATGAGCTGAGGAGCTGAG	1993						
Qy	3195	GAATCTCTCTGAGGCTCTGAGTGTGAACTCTGAGCTTATGAGTA	3254						
Db	1994	GAATCTCTCTGAGGCTCTGAGTGTGAACTCTGAGCTTATGAGTA	2153						
Qy	3255	CCCAAACCTCTCTGCGGCTGCGGCTGAGCTGAGCTGAGCTG	3114						
Db	2054	CCCAAACCTCTCTGCGGCTGCGGCTGAGCTGAGCTGAGCTG	2113						
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QY	/ab_xref="Taxon: 9606"
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QY	1321 CCATGCTATCGTCAGCAGCTGTGGCTGGATCCAGAGACTACTAGTGTGGAGA 2708
Db	2649 CCACTTCCACTTCTGCTCAGAGCTACTAGCTGGGAGAGCGGGCTCTGCCTCTGCTCAGGGCTACTA 1320
QY	2709 ACCCAAGCTAATCTGCTGCAATTCTCCTGAGCAGAGTCACCATCTGCTGGAGA 2708
Db	1381 ACCCAAGCTAATCTGCTGCAATTCTCCTGAGCAGAGTCACCATCTGCTGGAGA 1380
QY	1441 CATAGATTCTGGCTGAAGTGGGCATCTCTGAGGACACTGACTGCATCTGCTC 2768
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Db	1801 GAGAGCAGCTCCCTACCTGCTGAGACATCTTACCCAGGAAAGTCACT 3156
QY	3157 GCGATTTGGTGCAGCAGCTCTGCTCACCTGCTGAGACATCTTACCCAGGAAAGTCACT 1860
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RCRANISM	Homo sapiens
ERENCE	Euarkyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; 1 (bases 1 to 1717)
SCHEIT, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and Pilarsky, C.	Human nucleic acid sequences of endometrium tumour tissue
PATENT:	WO 954461-A 11 28-OCT-1995;
SCHEIT, ARMIN (DE); SPECHT, THOMAS (DE); DAHL, EDGAR (DE); HINZMANN, BERND (DE); ROSENTHAL, ANDRE (DE); METAGEN GES FUER GENOMFORSCHUNG (DE); PILARSKY, CHRISTIAN (DE)	Location/Qualifiers

QY	1243	CCCTGCCCATATGGTTCCTACTCCAAATGGCTCAGACTGTTACCGCTGCGCTCAGGGACT	1302	Db	
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Qy	1303	GAACCTGCTGGGATTGAACTACAATGGGACACGGCTGCCAACACATGGAAAC	1362	Db	
Db	901	ACCGTCTCTAGGGTCACTCTGAGTACAGCTGAGTACAGGGTGAACGGCTGGGGCTGT	960	Qy	
Qy	1423	GATCACATTTCACACAGCTGCTGAGGCTGAGCTGAGAATGAAAGGTGCC	1482	Db	
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Qy	1483	GTGCCAGGATTAGACCTCCGACTGGTGTGGATGAGACAGAGATAAGGGTCCC	1542	Db	
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ACCESSION	AX213277				
AUTHORS	Glucksmann, M.A. and Silos-Santiago, I.				
TITLE	Seven-transmembrane proteins/g-protein coupled receptors				
JOURNAL	Patent: WO 0159117-A 7 16-AUG-2001; Millennium Pharmaceuticals, Inc. (US)				
FEATURES	Location/qualifiers				
source	1. .1587				
ORGANISM	Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
REFERENCE	1 (bases 1 to 1587)				
AUTHORS	Glucksmann, M.A. and Silos-Santiago, I.				
TITLE	Seven-transmembrane proteins/g-protein coupled receptors				
JOURNAL	Patent: WO 0159117-A 7 16-AUG-2001; Millennium Pharmaceuticals, Inc. (US)				
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ORIGIN					
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Best Local Similarity	99..3%	Pred. No. 2e-247;	Length 1587;		
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Matches	1013;	Conservative 0;	Mismatches 7;	Indels 0;	
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DEFINITION	Sequence 9 from Patent WO0159117.		PAT	06-SEP-2001	
ACCESSION	AX213279				
VERSION	AX213279..1				
FEATURES	source				
ORGANISM	Homo sapiens				

ORIGIN

Query Match 25.0%; Score 834.4; DB 10; Length 1149;
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 Matches 978; Conservative 0; Mismatches 161; Indels 7; Gaps 4;
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RESULT 15

DEFINITION Homo sapiens cDNA FLJ31340 3195 bp mRNA Linear PRI 01-AUG-2002
 TO MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR.
 ACCESSION AK055902
 VERSION AK055902.1 GI:1550745
 KEYWORDS oligo capping; LIS (full insert sequence); Homo sapiens; normal mesangial cells; (NINM56046-2); cDNA to mRNA;
 SOURCE clone; lib:ME3AN1 clone:ME3AN100035.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE AK055902
 AUTHORS Toshiro.H., Yamazaki.M., Watanabe.K., Kumagai.A., Itakura.S., Fukuzumi.Y., Fujimori.Y., Komiyama.M., Sugiyama.T., Irie.R., Isobe.Y., Otsuki.T., Sato.H., Wakamatsu.A., Iishi.S., Yamamoto.J., Isobe.Y., Kawai-Hio.Y., Saito.K., Nishikawa.T., Kimura.T., Yamashita.H., Matsuo.K., Nakamura.Y., Sekine.M., Kikuchi.H., Kanda.K., Wagatsuma.M., Murakawa.K., Konehori.K., Takahashi-Fujii.K., Oshima.A., Sugiyama.A., Kawakami.B., Suzuki.Y., Sugano.S., Nagahara.K., Masuhara.Y., Nagai.K. and Isogai.T.

TITLE Homo sapiens cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3185)
 AUTHORS Isogai.T., Otsuki.T. and Sugiyama.T.

JOURNAL Direct Submission
 SUBMITTED 24-OCT-2001 Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology (RAB); cDNA library construction; Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing; RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing; RAB and HRI.

FEATURES Location/Ouflifiers

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